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07/7 #6

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/043,344

DATE: 07/18/2002

TIME: 11:09:30

Input Set : A:\10043341.APP.txt

Output Set: N:\CRF3\07182002\J043344.raw

3 <110> APPLICANT: Loosmore, Sheena M.
4 Harkness, Robin E.
5 Schryvers, Anthony B.
6 Chong, Pele
7 Gray-Owen, Scott
8 Murdin, Andrew D.
9 Klein, Michel H.
11 <120> TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
13 <130> FILE REFERENCE: 1038-1221 MIS
15 <140> CURRENT APPLICATION NUMBER: 10/043,344
C--> 16 <141> CURRENT FILING DATE: 2002-07-01
18 <150> PRIOR APPLICATION NUMBER: 08/649,518
19 <151> PRIOR FILING DATE: 1996-05-17
21 <160> NUMBER OF SEQ ID NOS: 160
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 4699
27 <212> TYPE: DNA
28 <213> ORGANISM: Haemophilus influenzae
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41 1 5 10
43 cta agt gct tgt agc gga ggg ggg tct ttt gat gta gat aac gtc tct 99
44 Leu Ser Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val Ser
45 15 20 25 30
47 aat acc ccc tct tct aaa cca cgt tat caa gac gat act tca agt tca 147
48 Asn Thr Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Ser
49 35 40 45
51 aga aca aaa tct aaa ttg gaa aag ttg tcc att cct tct tta ggg gga 195
52 Arg Thr Lys Ser Lys Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly
53 50 55 60
55 ggg atg aag tta gcg gct ctg aat ctt ttt gat agg aac aaa cct agt 243
56 Gly Met Lys Leu Ala Ala Leu Asn Leu Phe Asp Arg Asn Lys Pro Ser
57 65 70 75
59 ctc tta aat gaa gat agc tat atg ata ttt tcc tca cgt tct acg att 291
60 Leu Leu Asn Glu Asp Ser Tyr Met Ile Phe Ser Ser Arg Ser Thr Ile

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63 gaa gag gat gtt aaa aat gac aat caa aac ggc gag cac cct att gac 339
64 Glu Glu Asp Val Lys Asn Asp Asn Gln Asn Gly Glu His Pro Ile Asp
65 95      100      105      110
67 tca ata gtc gat cct aga gca cca aat tca aac gaa aat cgt cat gga 387
68 Ser Ile Val Asp Pro Arg Ala Pro Asn Ser Asn Glu Asn Arg His Gly
69      115      120      125
71 caa aaa tat gta tat tca ggg ctt tat tat att caa tcg tgg agt cta 435
72 Gln Lys Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Ser Leu
73      130      135      140
75 aga gat tta cca aat aaa aag ttt tat tca ggt tac tat gga tat gcg 483
76 Arg Asp Leu Pro Asn Lys Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr Ala
77      145      150      155
79 tat tac ttt ggc aat aca act gcc tct gca tta cct gta ggt ggc gta 531
80 Tyr Tyr Phe Gly Asn Thr Thr Ala Ser Ala Leu Pro Val Gly Gly Val
81      160      165      170
83 gca acg tat aaa gga act tgg agc ttc atc acc gca gct gaa aat ggc 579
84 Ala Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Ala Glu Asn Gly
85 175      180      185      190
87 aag aat tat gaa ttg tta aga aat tct ggt ggc ggt caa gct tat tct 627
88 Lys Asn Tyr Glu Leu Arg Asn Ser Gly Gly Gly Gln Ala Tyr Ser
89      195      200      205
91 cga cgt agt gct act cca gaa gat att gat tta gat cgt aag acg ggc 675
92 Arg Arg Ser Ala Thr Pro Glu Asp Ile Asp Leu Asp Arg Lys Thr Gly
93      210      215      220
95 tta aca agt gaa ttt act gtc aat ttt ggt aca aaa aag ctc act gga 723
96 Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr Gly
97      225      230      235
99 gga ctt tat tat aat tta cgt gaa aca gat gct aat aaa tca caa aat 771
100 Gly Leu Tyr Tyr Asn Leu Arg Glu Thr Asp Ala Asn Lys Ser Gln Asn
101      240      245      250
103 aga aca cat aaa ctc tac gat cta gaa gct gat gtt cat agc aac cga 819
104 Arg Thr His Lys Leu Tyr Asp Leu Glu Ala Asp Val His Ser Asn Arg
105 255      260      265      270
107 ttc agg ggt aaa gta aag cca acc aaa aaa gag tct tct gaa gaa cat 867
108 Phe Arg Gly Lys Val Lys Pro Thr Lys Lys Glu Ser Ser Glu Glu His
109      275      280      285
111 ccc ttt acc agc gag gga aca tta gaa ggt ggt ttt tac ggg cct gag 915
112 Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Glu
113      290      295      300
115 ggt caa gaa tta gga gga aag ttt tta gct cac gac aaa aaa gtt ttg 963
116 Gly Gln Glu Leu Gly Gly Lys Phe Leu Ala His Asp Lys Lys Val Leu
117      305      310      315
119 ggg gta ttt agt gcc aaa gaa cag caa gaa acg tca gaa aac aaa aaa 1011
120 Gly Val Phe Ser Ala Lys Glu Gln Gln Glu Thr Ser Glu Asn Lys Lys
121      320      325      330
123 tta ccc aaa gaa acc tta att gat ggc aag cta act act ttt aaa aca 1059
124 Leu Pro Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Lys Thr
125 335      340      345      350

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127 acc aat gca aca gcc aat gca aca acc gat gca aca acc agt aca aca 1107
128 Thr Asn Ala Thr Ala Asn Ala Thr Thr Asp Ala Thr Thr Ser Thr Thr
129 355 360 365
131 gcc agt aca aaa acc gat aca aca acc aat gca aca gcc aat aca gaa 1155
132 Ala Ser Thr Lys Thr Asp Thr Thr Thr Asn Ala Thr Ala Asn Thr Glu
133 370 375 380
135 aac ttt acg aca aaa gat ata cca agt ttg ggt gaa gct gat tat ctt 1203
136 Asn Phe Thr Thr Lys Asp Ile Pro Ser Leu Gly Glu Ala Asp Tyr Leu
137 385 390 395
139 tta att gat aat tac cct gtt cct ctt ttc cct gag agt ggt gat ttc 1251
140 Leu Ile Asp Asn Tyr Pro Val Pro Leu Phe Pro Glu Ser Gly Asp Phe
141 400 405 410
143 ata agt agt aag cac cat act gta gga aag aaa acc tat caa gta gaa 1299
144 Ile Ser Ser Lys His His Thr Val Gly Lys Lys Thr Tyr Gln Val Glu
145 415 420 425 430
147 gca tgt tgc agt aat cta agc tat gta aaa ttt ggt atg tat tat gaa 1347
148 Ala Cys Cys Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu
149 435 440 445
151 gcc cca cct aaa gaa gaa gaa aaa gaa aaa gaa aaa gac aaa gac aaa 1395
152 Ala Pro Pro Lys Glu Glu Glu Lys Glu Lys Glu Lys Asp Lys Asp Lys
153 450 455 460
155 gaa aaa gaa aaa caa gcg aca aca tct atc aag act tat tat caa ttc 1443
156 Glu Lys Glu Lys Gln Ala Thr Thr Ser Ile Lys Thr Tyr Tyr Gln Phe
157 465 470 475
159 tta tta ggt ctc cgt act ccc agt tct gaa ata cct aaa gaa gga agt 1491
160 Leu Leu Gly Leu Arg Thr Pro Ser Ser Glu Ile Pro Lys Glu Gly Ser
161 480 485 490
163 gca aaa tat cat ggt aat tgg ttt ggt tat att agt gat ggc gag aca 1539
164 Ala Lys Tyr His Gly Asn Trp Phe Gly Tyr Ile Ser Asp Gly Glu Thr
165 495 500 505 510
167 tct tac tcc gcc agt ggt gat aag gaa cgc agt aaa aat gct gtc gcc 1587
168 Ser Tyr Ser Ala Ser Gly Asp Lys Glu Arg Ser Lys Asn Ala Val Ala
169 515 520 525
171 gag ttt aat gta aat ttt gcc gag aaa aca tta aca ggc gaa tta aaa 1635
172 Glu Phe Asn Val Asn Phe Ala Glu Lys Thr Leu Thr Gly Glu Leu Lys
173 530 535 540
175 cga cac gat act caa aat ccc gta ttt aaa att aat gca acc ttt caa 1683
176 Arg His Asp Thr Gln Asn Pro Val Phe Lys Ile Asn Ala Thr Phe Gln
177 545 550 555
179 agt ggt aag aat gac ttc act ggt aca gca acc gca aaa gat tta gca 1731
180 Ser Gly Lys Asn Asp Phe Thr Gly Thr Ala Thr Ala Lys Asp Leu Ala
181 560 565 570
183 ata gat ggt aaa aat aca caa ggc aca tct aaa gtc aat ttc acg gca 1779
184 Ile Asp Gly Lys Asn Thr Gln Gly Thr Ser Lys Val Asn Phe Thr Ala
185 575 580 585 590
187 aca gta aac ggg gca ttt tat ggt ccg cac gct aca gaa tta ggc ggt 1827
188 Thr Val Asn Gly Ala Phe Tyr Gly Pro His Ala Thr Glu Leu Gly Gly
189 595 600 605
191 tat ttc acc tat aac gga aac aat cct aca gat aaa aat tca tca tcc 1875

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196 Asn Ser Glu Lys Ala Arg Ala Val Val Phe Gly Ala Lys Lys Gln
197      625      630      635
199 caa gta gaa aca acc aa gtaatggaat actaaa a atg act aaa aaa ccc 1972
200 Gln Val Glu Thr Thr Lys      Met Thr Lys Lys Pro
201      640      645
203 tat ttt cgc cta agt att att tct tgt ctt tta att tca tgc tat gta 2020
204 Tyr Phe Arg Leu Ser Ile Ile Ser Cys Leu Leu Ile Ser Cys Tyr Val
205 650      655      660      665
207 aaa gca gaa act caa agt ata aaa gat aca aaa gaa gct ata tca tct 2068
208 Lys Ala Glu Thr Gln Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser Ser
209      670      675      680
211 gaa gtg gac act caa agt aca gaa gat tca gaa tta gaa act atc tca 2116
212 Glu Val Asp Thr Gln Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile Ser
213      685      690      695
215 gtc act gca gaa aaa gtt aga gat cgt aaa gat aat gaa gta act gga 2164
216 Val Thr Ala Glu Lys Val Arg Asp Arg Lys Asp Asn Glu Val Thr Gly
217      700      705      710
219 ctt ggc aaa att ata aaa act agt gaa agt atc agc cga gaa caa gta 2212
220 Leu Gly Lys Ile Ile Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln Val
221      715      720      725
223 tta aat att cgt gat cta aca cgc tat gat cca ggg att tca gtt gta 2260
224 Leu Asn Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val
225 730      735      740      745
227 gaa caa ggt cgc ggt gca agt tct gga tat tct att cgt ggt atg gac 2308
228 Glu Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp
229      750      755      760
231 aga aat aga gtt gct tta tta gta gat ggt tta cct caa acg caa tct 2356
232 Arg Asn Arg Val Ala Leu Leu Val Asp Gly Leu Pro Gln Thr Gln Ser
233      765      770      775
235 tat gta gtg caa agc cct tta gtt gct cgt tca gga tat tct ggc act 2404
236 Tyr Val Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr
237      780      785      790
239 ggt gca att aat gaa att gaa tat gaa aat gta aag gcc gtc gaa ata 2452
240 Gly Ala Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile
241      795      800      805
243 agc aag ggg ggg agt tct tct gag tat ggt aat gga gca cta gct ggt 2500
244 Ser Lys Gly Gly Ser Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly
245 810      815      820      825
247 tct gta aca ttt caa agc aaa tca gca gcc gat atc tta gaa gga gac 2548
248 Ser Val Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp
249      830      835      840
251 aaa tca tgg gga att caa act aaa aat gct tat tca agc aaa aat aaa 2596
252 Lys Ser Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys
253      845      850      855
255 ggc ttt acc cat tct tta gct gta gca gga aaa caa ggt gga ttt gaa 2644
256 Gly Phe Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Gly Phe Glu

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260	Gly Val Ala Ile Tyr Thr His Arg Asn Ser Ile Glu Thr Gln Val His			
261	875	880	885	
263	aaa gat gca tta aaa ggc gtg caa agt tat gat cga ttc atc gcc aca	2740		
264	Lys Asp Ala Leu Lys Gly Val Gln Ser Tyr Asp Arg Phe Ile Ala Thr			
265	890	895	900	905
267	aca gag gat caa tct gca tac ttt gtg atg caa gat gag tgt cta gat	2788		
268	Thr Glu Asp Gln Ser Ala Tyr Phe Val Met Gln Asp Glu Cys Leu Asp			
269	910	915	920	
271	ggt tat gac aag tgt aaa act tca ccc aaa cga cct gcg act tta tcc	2836		
272	Gly Tyr Asp Lys Cys Lys Thr Ser Pro Lys Arg Pro Ala Thr Leu Ser			
273	925	930	935	
275	acc caa aga gaa acc gta agc gtt tca gat tat acg ggg gct aac cgt	2884		
276	Thr Gln Arg Glu Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg			
277	940	945	950	
279	atc aaa cct aat cca atg aaa tat gaa agc cag tct tgg ttt tta aga	2932		
280	Ile Lys Pro Asn Pro Met Lys Tyr Glu Ser Gln Ser Trp Phe Leu Arg			
281	955	960	965	
283	gga ggt tat cat ttt tct gaa caa cac tat att ggt ggt att ttt gaa	2980		
284	Gly Gly Tyr His Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe Glu			
285	970	975	980	985
287	ttc aca caa caa aaa ttt gat atc cgt gat atg aca ttt ccc gct tat	3028		
288	Phe Thr Gln Gln Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr			
289	990	995	1000	
291	tta agg cca aca gaa gac aag gat tta caa agt cgc cct ttt tat cca	3076		
292	Leu Arg Pro Thr Glu Asp Lys Asp Leu Gln Ser Arg Pro Phe Tyr Pro			
293	1005	1010	1015	
295	aag caa gat tat ggt gca tat caa cat att ggt gat ggc aga ggc gtt	3124		
296	Lys Gln Asp Tyr Gly Ala Tyr Gln His Ile Gly Asp Gly Arg Gly Val			
297	1020	1025	1030	
299	aaa tat gca agt ggg ctt tat ttc gat gaa cac cat aga aaa cag cgt	3172		
300	Lys Tyr Ala Ser Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln Arg			
301	1035	1040	1045	
303	gta ggt att gaa tat att tac gaa aat aag aac aaa gcg ggc atc att	3220		
304	Val Gly Ile Glu Tyr Ile Tyr Glu Asn Lys Asn Lys Ala Gly Ile Ile			
305	1050	1055	1060	1065
307	gac aaa gcg gtg tta agt gct aat caa caa aca tca tac ttg aca gtt	3268		
308	Asp Lys Ala Val Leu Ser Ala Asn Gln Gln Thr Ser Tyr Leu Thr Val			
309	1070	1075	1080	
311	ata tgc gac ata cgc att gca gtc ttt atc cat aat cca agt aag aat	3316		
312	Ile Cys Asp Ile Arg Ile Ala Val Phe Ile His Asn Pro Ser Lys Asn			
313	1085	1090	1095	
315	tgc cgc cca aca ctt gat aaa cct tat tca tac tat cat tct gat aga	3364		
316	Cys Arg Pro Thr Leu Asp Lys Pro Tyr Ser Tyr Tyr His Ser Asp Arg			
317	1100	1105	1110	
319	aat gtt tat aaa gaa aaa cat aac atg ttg caa ttg aat tta gag aaa	3412		
320	Asn Val Tyr Lys Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu Lys			
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VERIFICATION SUMMARY

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date